

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti  
Shah, Purvi  
Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN MEMBRANE RECYCLING  
PROTEINS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Dr.  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/360,125  
(B) FILING DATE: July 23, 1999

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/004,502  
(B) FILING DATE: January 8, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0456 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: TONGTUT01  
(B) CLONE: 980615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Ser | Arg | Asp | Gly | Gly | Asn | Pro | Phe | Ala | Glu | Pro | Ser | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Asp | Asn | Pro | Phe | Gln | Asp | Pro | Ala | Val | Ile | Gln | His | Arg | Pro | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Arg | Gln | Tyr | Ala | Thr | Leu | Asp | Val | Tyr | Asn | Pro | Phe | Glu | Thr | Arg | Glu |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Pro | Pro | Ala | Tyr | Glu | Pro | Pro | Ala | Pro | Ala | Pro | Leu | Pro | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Pro | Ser | Leu | Gln | Pro | Ser | Arg | Lys | Leu | Ser | Pro | Thr | Glu | Pro |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asn | Tyr | Gly | Ser | Tyr | Ser | Thr | Gln | Ala | Ser | Ala | Ala | Ala | Ala | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |
| Ala | Glu | Leu | Leu | Lys | Lys | Gln | Glu | Glu | Leu | Asn | Arg | Lys | Ala | Glu | Glu |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |
| Leu | Asp | Arg | Arg | Glu | Arg | Glu | Leu | Gln | His | Ala | Ala | Leu | Gly | Gly | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Thr | Arg | Gln | Asn | Asn | Trp | Pro | Pro | Leu | Pro | Ser | Phe | Cys | Pro | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Pro | Cys | Phe | Phe | Gln | Asp | Ile | Ser | Met | Glu | Ile | Pro | Gln | Glu | Phe |
|     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Lys | Thr | Val | Ser | Thr | Met | Tyr | Tyr | Leu | Trp | Met | Cys | Ser | Thr | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Leu | Leu | Asn | Phe | Leu | Ala | Cys | Leu | Ala | Ser | Phe | Cys | Val | Glu |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Thr | Asn | Asn | Gly | Ala | Gly | Phe | Gly | Leu | Ser | Ile | Leu | Trp | Val | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Thr | Pro | Cys | Ser | Phe | Val | Cys | Trp | Tyr | Arg | Pro | Met | Tyr | Lys | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Arg | Ser | Asp | Ser | Ser | Phe | Asn | Phe | Phe | Val | Phe | Phe | Phe | Ile | Phe |
|     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Val | Gln | Asp | Val | Leu | Phe | Val | Leu | Gln | Ala | Ile | Gly | Ile | Pro | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Trp | Gly | Phe | Ser | Gly | Trp | Ile | Ser | Ala | Leu | Val | Val | Pro | Lys | Gly | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Ala | Val | Ser | Val | Leu | Met | Leu | Leu | Val | Ala | Leu | Leu | Phe | Thr | Gly |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Ala | Val | Leu | Gly | Ile | Val | Met | Leu | Lys | Arg | Ile | His | Ser | Leu | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Arg | Thr | Gly | Ala | Ser | Phe | Gln | Lys | Ala | Gln | Gln | Glu | Phe | Ala | Ala |
|     | 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Val | Phe | Ser | Asn | Pro | Ala | Val | Arg | Thr | Ala | Ala | Ala | Asn | Ala | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Gly | Ala | Ala | Glu | Asn | Ala | Phe | Arg | Ala | Pro |     |     |     |     |     |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TONGTUT01
- (B) CLONE: 980615

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| NGACGCGAGC  | GCAACCCACG  | GCTGCTGCGG | GGATCCTTGT  | GGCCCTTCCG | GTCTGATGGA | 60  |
| CCAATCCGTG  | CACAGAGAAG  | CGGGGCGAAG | TGAGGCGAGT  | GAAGTGGACT | CTGAGGGGTA | 120 |
| CCGCTACCGC  | CACTGCTGCG  | GCAGGGGCGT | GGAGGGGAGA  | GGGCCGCGGA | GGCCGCGAGT | 180 |
| GCAAACATGG  | CTCAGAGCAG  | AGACGGCGGA | AACCCGTTCG  | CCGAGCCGAG | CGAGCTTGAC | 240 |
| AACCCCTTTC  | AGGACCCAGC  | TGTGATCCAG | CACCGACCCA  | GCCGGCAGTA | TGCCACGCTT | 300 |
| GACGCTCTACA | ACCCTTTTGA  | GACCCGGGAG | CCACCACCCG  | CCTATGAGCC | TCCAGCCCTT | 360 |
| GCCCCATTTGC | CTCCACCCCTC | AGCTCCCTCC | TTCGAGCCCT  | CGAGAAAGCT | CAGCCCCACA | 420 |
| GAACCTAAGA  | ACTATGCTC   | ATACAGCACT | CAGGCCCTCAG | CTGCAGCAGC | CACAGCTGAG | 480 |
| CTGCTGAAGA  | AACAGGAGGA  | GCTCAACCGG | AAGGCAGAGG  | AGTTGGACCG | AAGGGAGCGA | 540 |
| GAGCTGCAGC  | ATGCTGCCCT  | GGGGGGCACA | GCTACTCGAC  | AGAACAATTG | GCCCTCTCTA | 600 |
| CCTTCTTTTT  | GTCCAGTTCA  | GCCTTGCTTT | TTCCAGGACA  | TCTCCATGGA | GATCCCCCAA | 660 |

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GAATTCAGAGAGACTGTATC CACCATGTAC TACCTCTGGA TGTGCAGCAC GCTGGCTCTT 720
CTCTGAACT TCCTCGCCTG CCTGGCCAGC TTCTGTGTGG AAACCAACAA TGGCGCAGGC 780
TTTGGGCTTT CTATCCTCTG GGTCTCTCTT TTAACCTCCT GTCCTTTTGT CTGCTGGTAC 840
CGCCCCATTT ATAAGGCTTT CCGGAGTGAC AGTTCATTTA ATTCTCTCGT TTCTCTCTTC 900
ATTTTCTTTCG TCCAGGATGT GCTCTTTGTC CTCCAGGCCA TTGGTATCCC AGGTTGGGGA 960
TTCACTGGCT GGATCTCTGC TCTGGTGGTG CCGAAGGGCA ACACAGCAGT ATCCGTGCTC 1020
ATGCTGTGCTG TCGCCCTGCT CTTCACGTGC ATTGCTGTGC TAGGAATTGT CATGCTGAAA 1080
CGGATCCACT CCTATATACC CGCACAGGT GCCAGCTTTC AGAAGGCCCA GCAAGAAATT 1140
GCTGCTGGTG TCTTCTCCAA CCCTGCGGTG CGAACCGCAG CTGCCAATGC AGCCGTGGG 1200
GCTGCTGAAA ATGCTCTCCG GCGCCCGTGA CCCCTGACTG GGATGCCCTG GCCCTGCTAC 1260
TTGAGGGAGC TGACTTAGCT CCGCTCCCTA AGGTCTCTGG GACTTGGAGA GACATCACTA 1320
ACTGATGGCT CTCCCGTAGT GCTCCCAATC CTATGCCCAT GACTGCTGAA CCTGACAGGC 1380
GTGTGGGGAG TTCACTGTGA CCTAGTCCCC CCATCAGGCC ACACCTGCTC CACCTCTCAC 1440
ACGCCCAAC ACAGCTTCCC TCTGCTGTGC CACGGCTGTT GCTTCGGTTA TTTAAATAAA 1500
AAGAAAGTGG AACGTGAACT G

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT01  
 (B) CLONE: 412453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Ser Ala Phe Asp Thr Asn Pro Phe Ala Asp Pro Val Asp Val Asn
1      5      10      15
Pro Phe Gln Asp Pro Ser Val Thr Gln Leu Thr Asn Ala Pro Gln Gly
20     25     30
Gly Leu Ala Glu Phe Asn Pro Phe Ser Glu Thr Asn Ala Ala Thr Thr
35     40     45
Val Pro Val Thr Gln Leu Pro Gly Ser Ser Gln Pro Ala Val Leu Gln
50     55     60
Pro Ser Val Glu Pro Thr Gln Pro Thr Pro Gln Ala Val Val Ser Ala
65     70     75     80
Ala Gln Ala Gly Leu Leu Arg Gln Gln Glu Glu Leu Asp Arg Lys Ala
85     90     95
Ala Glu Leu Glu Arg Lys Glu Arg Glu Leu Gln Asn Thr Val Ala Asn
100    105    110
Leu His Val Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Trp Cys Pro
115    120    125
Val Lys Pro Cys Phe Tyr Gln Asp Phe Ser Thr Glu Ile Pro Ala Asp
130    135    140
Tyr Gln Arg Ile Cys Lys Met Leu Tyr Tyr Leu Trp Met Leu His Ser
145    150    155    160
Val Thr Leu Phe Leu Asn Leu Leu Ala Cys Leu Ala Trp Phe Ser Gly
165    170    175
Asn Ser Ser Lys Gly Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
180    185    190
Ile Phe Thr Pro Cys Ala Phe Leu Cys Trp Tyr Arg Pro Ile Tyr Lys
195    200    205
Ala Phe Arg Ser Asp Asn Ser Phe Ser Phe Val Phe Phe Phe Val
210    215    220
Phe Phe Cys Gln Ile Gly Ile Tyr Ile Ile Gln Leu Val Gly Ile Pro
225    230    235    240
Gly Leu Gly Asp Ser Gly Trp Ile Ala Ala Leu Ser Thr Leu Asp Asn
245    250    255
His Ser Leu Ala Ile Ser Val Ile Met Met Val Val Ala Gly Phe Phe
260    265    270
Thr Leu Cys Ala Val Leu Ser Val Phe Leu Leu Gln Arg Val His Ser
275    280    285
Leu Tyr Arg Arg Thr Gly Ala Ser Phe Gln Gln Ala Gln Glu Glu Phe

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|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 290                     | 295                 | 300                 |
| Ser Gln Gly Ile Phe Ser | Ser Arg Thr Phe His | Arg Ala Ala Ser Ser |
| 305                     | 310                 | 315                 |
| Ala Ala Gln Gly Ala Phe | Gln Gly Asn         |                     |
| 325                     |                     |                     |

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2434 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT01  
 (B) CLONE: 412453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| NCCGGAAGTG | GAGGGTCTAC  | ACGAAGCGCC  | GCTGGGCTCG  | GGTGCCCGGA  | GGCAGCAGCG  | 60   |
| TTCCGCGAGT | TCGCCCGCTG  | GCCCCCGATC  | ACCATGTCTG  | CTTTCGACAC  | CAACCCCTTC  | 120  |
| CGCGACCCAG | TGGATGTAAA  | CCCCCTCCAG  | GATCCCTCTG  | TGACCCAGCT  | GACCAACGCC  | 180  |
| CCGACGGCGC | GCCTGGCGGA  | ATTCAACCCC  | TTCTCAGAGA  | CAAAATGCAGC | GACAACAGTT  | 240  |
| CCTGTACCC  | AACCTCCCTGG | GTCCCTCACAG | CCAGCGGTTT  | TCCAGCCATC  | AGTGGAAACCA | 300  |
| ACCCAGCCGA | CCCCCAGGC   | CGTGGTGTCT  | GCAGCCGAGC  | CAGGCCCTGT  | CCGGCAGCAG  | 360  |
| GAAGAACTGG | ACGAGAAAGC  | TGCCGAGCTG  | GAACGCAAGG  | AGCGGGAGCT  | GCAGAACACT  | 420  |
| GTAGCCAACT | TACATGTGAG  | ACAGAACAAAC | TGGCCCCCTC  | TGCCCTCTGT  | GTGCCCTGTG  | 480  |
| AAGCCCTGCT | TCTATCAGGA  | TTTCTCCACA  | GAGATCCCTG  | CCGACTACCA  | CGCGATATGC  | 540  |
| AAGATGCTCT | ACTATCTGTG  | GATGTTGCAT  | TCAGTGACTC  | TGTTTCTGAA  | CTCGCTTGCC  | 600  |
| TGCCCTGCTC | GGTTCTCGGG  | CAACAGCTCC  | AAGGGAGTGG  | ACTTTGGCCT  | CTCCATCTGT  | 660  |
| TGGTTCTCTA | TCTTCACTCC  | CTGTGCCCTT  | CTTTGTTGGT  | ACCGACCCAT  | CTATAAGGCC  | 720  |
| TTTAGGTCG  | ACAACCTCTT  | CAGCTTCTTT  | GTGTCTCTCT  | TGTATTTTTT  | TTGTCAAAAT  | 780  |
| GGGATCTACA | TCAATCAGTT  | GGTTGGCATC  | CCTGGCCTGG  | GGGACAGCGG  | TTGGATTGCA  | 840  |
| GGCCTGTCTA | CATGATATA   | TCATTCCCTG  | GCCATATCAG  | TCATCATGAT  | GGTGGTGCGT  | 900  |
| GGCTTCTCTA | CCCTCTGTGC  | CGTCTCTCTA  | GTCTTCTCTC  | TGCAGCGGGT  | GCACTCCCTC  | 960  |
| TACCGACGGA | CAGGGGCGAG  | CTTCCAGCAG  | GCCCAGGAGG  | AGTTTTTCCA  | GGGCATCTTC  | 1020 |
| AGCAGCAGAA | CCTTCCACAG  | AGCTGCTTCA  | TCTGCTGCC   | AAGGAGCCTT  | CCAGGGGAAT  | 1080 |
| TAGTCTCTCT | CTCTTCTCTC  | CCCCTCAGCC  | TTTCTCTCGC  | CTGCCTTCTG  | AGCTGCACCT  | 1140 |
| TCCGTGGGTG | CTTTATGTGG  | TGTTGGTTGT  | GCCCAGCACA  | GACCTGGCAG  | GGTTCTTGCC  | 1200 |
| GTGGCTCTTC | CTCTCCCTTC  | AGGCACGAGC  | TCTCCCTTGA  | ACGGGAGGGA  | CAGGGAATTT  | 1260 |
| TTTCCCCCTC | TATGTACAAA  | AAAAAACAAA  | GCTCTCTTTC  | CTTCTCTGTT  | GATGGTTTGG  | 1320 |
| TAGGATTCTT | TTGTCTCTGG  | AAGCAGTGGG  | ACTGAAGTTT  | TCCTCGCTCT  | GTGCACACAC  | 1380 |
| AGACACCCCC | ACACAGTTGG  | GATCACAGGC  | TGACCTGGGC  | CCATCCGAGC  | TGGAGCTTTT  | 1440 |
| TGCCAGGGTG | TGGGGGCTTG  | ACTCCCCCAC  | CCTGCAGGCC  | TGGCCTGAAT  | CTGGCTTTCT  | 1500 |
| AGACACAGCC | CAGTCTTCC   | TGCCCTGGGT  | GGGAATAAGC  | CTCTCACAGC  | TTCTGTGGGA  | 1560 |
| CAGATCTGTT | CCCCAGGTCA  | CTCCAGTGGT  | CTCCAGGCTT  | CCAGAGAAGG  | CTGGTTGCTT  | 1620 |
| CAAGCTCTTC | TCTGCCTCAT  | AAACGGATCC  | AGAGAAGGCT  | GGTTGCTTCA  | AGCTCTTGCC  | 1680 |
| TGCCCTGCTG | TCCTGAGAAA  | CGGATTAAAT  | GCCCTTTATC  | CCCCTGACCC  | CTCCCTGCGG  | 1740 |
| CGATGGCTCT | TTGAGCCCTT  | TGGAGCCCTC  | CCCTTGCTGA  | GCCTTACTCT  | TTCCAGACTT  | 1800 |
| TCTGAATGTA | CAGTGGCGTT  | GGTTGGGATT  | TGGGGACTGG  | AAGGGACCAA  | GGACACTGAC  | 1860 |
| CCCCAAGCTT | CCTGCCTAGC  | GTCACGCTG   | TTCTAGGAGG  | GTGGGGTCTG  | CTGTCCTGTG  | 1920 |
| TGTGGTTGGT | TGCGCCTGT   | TTGCTGTGAC  | TACCCCCCCC  | CCTCCCCGAA  | CCGAGGGGAG  | 1980 |
| GCTGCTCTTT | TCTCTCCCTC  | AGATGCCACC  | TGCCCCGCC   | ATGCTCCCCA  | TACAGACGAT  | 2040 |
| CCAGACTTTT | AGGAAGGGCA  | GGACCAAGCA  | GTCACAGAACC | GCATCCCTCA  | CGAGGAGCTG  | 2100 |
| ATPAGCCACT | TCTCGAGGGC  | CCCCCTAATA  | CCAGTGGAGG  | TCTGGTTTCA  | ACCTTGGGGG  | 2160 |
| GTGTGTCAC  | GTGATGGGAC  | ACGTAGGAGT  | CCACCTTTAA  | AACCAAGACC  | CTGTCCCTCG  | 2220 |
| AGGCTGCGCA | GTGGGTGTGT  | GGACTGGGTT  | GCCTTCCACC  | AAAACAGCC   | TCCGGCTCTG  | 2280 |
| GGCCCGAGAC | AGCCGACAGC  | CCCAGCCACT  | GAATGATACT  | GGCAGCGGCT  | GGGGTTTTAT  | 2340 |
| GAACCTCTTT | CTGATATTTT  | TTCCCTCTTA  | TGTACAAATG  | TATATGTTAC  | GTCTCAATTT  | 2400 |
| TTGTGCTTAA | GTAATAATAA  | AAACATTTTC  | AGAC        |             |             | 2434 |

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GenBank  
(B) CLONE: 487057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
 1      5      10      15
Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
 20      25      30
Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
 35      40      45
Gly Gly Val Lys Met Pro Asn Val Pro Asn Thr Gln Pro Ala Ile Met
 50      55      60
Lys Pro Thr Glu Glu His Pro Ala Tyr Thr Gln Ile Thr Lys Glu His
 65      70      75      80
Ala Leu Ala Gln Ala Glu Leu Leu Lys Arg Gln Glu Glu Leu Glu Arg
 85      90      95
Lys Ala Ala Glu Leu Asp Arg Arg Glu Arg Glu Met Gln Asn Leu Ser
 100      105      110
Gln His Gly Arg Lys Asn Asn Trp Pro Pro Leu Pro Ser Asn Phe Pro
 115      120      125
Val Gly Pro Cys Phe Tyr Gln Asp Phe Ser Val Asp Ile Pro Val Glu
 130      135      140
Phe Gln Lys Thr Val Lys Leu Met Tyr Tyr Leu Trp Met Phe His Ala
 145      150      155      160
Val Thr Leu Phe Leu Asn Ile Phe Gly Cys Leu Ala Trp Phe Cys Val
 165      170      175
Asp Ser Ser Arg Ala Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
 180      185      190
Leu Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Leu Tyr Gly
 195      200      205
Ala Phe Arg Ser Asp Ser Ser Phe Arg Phe Phe Val Phe Phe Val
 210      215      220
Tyr Ile Cys Gln Phe Ala Val His Val Leu Gln Ala Ala Gly Phe His
 225      230      235
Asn Trp Gly Asn Cys Gly Trp Ile Ser Ser Leu Thr Gly Leu Asn Lys
 245      250      255
Asn Ile Pro Val Gly Ile Met Met Ile Ile Ala Ala Leu Phe Thr
 260      265      270
Ala Ser Ala Val Ile Ser Leu Val Met Phe Lys Lys Val His Gly Leu
 275      280      285
Tyr Arg Thr Thr Gly Ala Ser Phe Glu Lys Ala Gln Gln Glu Phe Ala
 290      295      300
Thr Gly Val Met Ser Asn Lys Thr Val Gln Thr Ala Ala Ala Asn Ala
 305      310      315      320
Ala Ser Thr Ala Ala Thr Ser Ala Ala Gln Asn Ala Phe Lys Gly Asn
 325      330      335
Gln Met

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